S/N unknown PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:	Chu, et al.	Serial No.:	unknown
Filed:	concurrent herewith	Docket No.:	7933.208USU1
Title:	SEQUENCING OF PEPTIDES BY MASS SPECTROMETRY		

CERTIFICATE UNDER 37 CFR 1.10
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By: 
Name: Brian Maharaj

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D. C. 20231

Dear Sir:

In connection with the above-identified application filed herewith, please enter the following preliminary amendment in accordance with 37 CFR 1.121, a copy of which is enclosed herewith:

IN THE CLAIMS

Please amend claim 3 as follows:

3. (AMENDED) A method according to claim 1 wherein the oligopeptide comprises from about 3 to about 10 amino acids.

Please amend claim 4 as follows:

4. (AMENDED) A method according to claim 1 wherein the silver is silver nitrate.

Please amend claim 5 as follows:

5. (AMENDED) A method according to claim 1 wherein the determination of partial sequence comprises searching for, and identifying cleaved amino acid residues based on differences in *m/z* values of neighboring triplets where the *m/z* value of the $[b_n - H + Ag]^+$ ion and the corresponding $[y_n + H + Ag]^+$ ion are related by the formula: $[y_n + H + Ag]^+ = [M + Ag]^+ + Ag^+ - [b_n - H + Ag]^+$.

Please amend claim 8 as follows:

8. (AMENDED) A method according to claim 1 wherein product ion spectra of the [M + Ag]$^+$ ion are collected under $E_{cm}s$, of 1.5, 2.0, 2.5 and 3.0 eV.

Please amend claim 9 as follows:

9. (AMENDED) A method according to claim 1 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.

Please amend claim 12 as follows:

12. (AMENDED) A method according to claim 10 wherein the searching and identifying is conducted by a custom search algorithm.

Please amend claim 14 as follows:

14. (AMENDED) A method according to claim 10 wherein product ion spectra of the [M + Ag]$^+$ ion are collected under $E_{cm}s$, of 1.5, 2.0, 2.5 and 3.0 eV.

Please amend claim 15 as follows:

15. (AMENDED) A method according to claim 10 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/ time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.

REMARKS

The above preliminary amendment is made to remove multiple dependencies from claims 3, 4, 5, 8, 9, 12, 14, and 15. Please refer to the Marked-Up claim pages 24, 25, and 26, attached herewith.

Applicants respectfully request that the preliminary amendment described herein be entered into the record prior to calculation of the filing fee and prior to examination and consideration of the above-identified application.

If a telephone conference would be helpful in resolving any issues concerning this communication, please contact Applicants' primary attorney-of record, Douglas P. Mueller (Reg. No. 30,300), at (612) 371.5237.

Respectfully submitted,

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Dated: March 13, 2001

By _____
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DPM/rw

WE CLAIM:

1. A method of analyzing argentinated peptides or proteins using mass spectrometry comprising:

(a) combining an oligopeptide with silver to provide a sample comprising argentiated oligopeptide;

(b) submitting the sample to a mass spectrometer;

(c) performing scans of silver containing peaks in optimum collision energies;

(d) identifying any doublet or triplet peak pattern;

(e) confirming with Y ions;

(f) determining partial sequence by the mass separation between two successive doublet or triplet pattern.

2. A method according to claim 1 wherein the performing scans comprises collecting product ion spectra of the $[M + Ag]^+$ ion, where M = oligopeptide;

3. A method according to claim 1 [or 2] wherein the oligopeptide comprises from about 3 to about 10 amino acids.

4. A method according to [any one of claims 1-3] wherein the silver is silver nitrate. ← CLAIM 1 --

5. A method according to [anyone of claims 1-4] wherein the determination of partial sequence comprises searching for, and identifying cleaved amino acid residues based on differences in *m/z* values of neighboring triplets where the *m/z* value of the $[b_n - H + Ag]^+$ ion and the corresponding $[y_n + H + Ag]^+$ ion are related by the formula: $[y_n + H + Ag]^+ = [M + Ag]^+ + Ag^+ - [b_n - H + Ag]^+$. ← CLAIM 1 --

6. A method according to claim 5 wherein the searching and identifying is conducted by a custom search algorithm.

7. A method according to claim 6 wherein the algorithm is written in

Visual Basic and looks for the triplet peak pattern of $(m/z)_1$, $(m/z)_2$ = $(m/z)_1$ – 18.0, and $(m/z)_3$ = $(m/z)_2$ – 28.0 as well as the doublet pattern of $(m/z)_2$ and (m/z)3, all to within ± 0.5 *m/z* unit.

8. A method according to anyone of claims 1-7 wherein product ion spectra of the $[M + Ag]^+$ ion are collected under E_{cm}s, of 1.5, 2.0, 2.5 and 3.0 eV.

9. A method according to anyone of claims 1-8 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.

10. A method of analyzing argentinated peptides or proteins using mass spectrometry comprising:

(a) combining an oligopeptide with silver nitrate in solution;

(b) submitting a sample of the solution to a mass spectrometer;

(c) collecting product ion spectra of the $[M + Ag]^+$ ion, where M = oligopeptide;

(d) identifying a triplet peak pattern;

(e) identifying a doublet peak pattern;

(f) searching for, and identifying cleaved amino acid residues based on differences in *m/z* values of neighboring triplets where the *m/z* value of the $[b_n - H + Ag]^+$ ion and the corresponding $[y_n + H + Ag]^+$ ion are related by the formula: $[y_n + H + Ag]^+ = [M + Ag]^+ + Ag^+ - [b_n - H + Ag]^+$.

11. A method according to claim 10 wherein the oligopeptide comprises from about 3 to about 10 amino acids.

12. A method according to claim 10 or 11 wherein the searching and identifying is conducted by a custom search algorithm.

13. A method according to claim 12 wherein the algorithm is written in Visual Basic and looks for the triplet peak pattern of $(m/z)_1$, $(m/z)_2$) = $(m/z)_1$ – 18.0, and $(m/z)_3$ = $(m/z)_2$ – 28.0 as well as the doublet pattern of $(m/z)_2$ and (m/z)3, all to within ± 0.5 *m/z* unit.

14. A method according to anyone of claims 10 to 13 wherein product ion spectra of the $[M + Ag]^+$ ion are collected under E_{cm}s, of 1.5, 2.0, 2.5 and 3.0 eV.

15. A method according to anyone of claims 10-14 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.